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GenCore version 5.1.6
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OM protein . protein search, using sw model

August 28, 2003, 18:28:57; Search time 11.2727 Seconds (Without alignments) 102.373 Million cell updates/sec Run on:

US-09-743-225-8 58

1 NTLKTPRVGGXA 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	methyl coenzyme M	methyl coenzyme M	probable membrane	DNA-directed DNA p	N-acetylglucosamin	F3H9.15 protein -	methyl coenzyme M	hypothetical prote	hypothetical prote	yaeB protein - Esc	conserved hypothet	hypothetical prote	tartrate dehydroge	undecaprenyl-phosp	phosphoglycerate d	D-3-phosphoglycera	D-3-phosphoglycera	phosphoglycerate d	inward rectifier p	pristinamycin I sy	ပု	hypothetical prote	3-isopropylmalate	regulatory protein	D-3-phosphoglycera	hypothetical prote	sugar transport pe	hypothetical prote	phosphoribosylform
																			-											
																		,												
	a	F69022	A28544	\$57385	DJBPT7	G86767	H86407	A64310	E90653	E85504	C64744	AG0532	T34260	F83783	H70346	DEECPG	D85947	H91101	AC0112	T29652	T30288	JC2466	T04718	849786	A26499	C82072	H82642	C87130	D85359	SYBS2G
	DB		N	~	ч	N	~	~	~	~		~	~	~	~	Н	~	~1	N	N	~	N	7	Н	~	~	~	~	N	-
	Length	443	443	991	704	257	266	451	235	235	235	235	310	353	357	410	410	410	413	514	2591	352	365	371	377	409	441	446	644	742
æ	Query	67.2	67.2	65.5	63.8	62.1	62.1	62.1	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6
	Score	39	39	38	37	36	36	36	35	35	35	35	35	35	35	35	35	35	35	35	35	34	34	34	34.	34	34	34	34	34
	Result No.	-	~	ო	4	ស	9	7	æ	σ	10	11	13	13	14	15	16	17	18	19	50	71	22	23	24	25	56	27	, 28	53

RESULT 2 A28544 methyl coenzyme M reductase (EC 1.8...-) I beta chain - Methanobacterium thermoautotr

cellulose 1,4-beta hypothetical prote	hypothetical prote hypothetical prote hypothetical prote hypothetical prote	probable ORFZ prot hypothetical prote conserved hypothet	probable extragent probable cell cycl glycoprotein gp63	rfe protein - Myco probable glycosylt protein secretion probable rfe prote	
S59077 142707	T28125 B70233 E86183 F97542	G71114 E75046 E82701	H70530 T41543 VGBE63	T09982 C87051 S64729 B70774	
000	9999	000	464	9999	
1090	2329 169 198 239	263 263 267	290 336 350	3998 4009 4004	
58.6 58.6	0 0 0 0 0 0 0	0.00 0.00 0.00	56.9 9.6.9	20.00 0.00 0.00	
8 8 4 4		, e, e, e,	8 8 8 8 8		
30 31	w w w w ∨ w 4 π	9 8 8 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	3 4 4 1 1 1	4 4 4 4 2 6 4 6	

## ALIGNMENTS

	RESULT 1 F69022 methyl coenzyme M reductase (EC 1.8) I beta chain - M C.Species: Methanobacterium thermoautotrophicum A:Variety: strain Delta H	chain - Methanobacterium thermoautotr
	C.Date: 05-Dec-1997 #sequence_revision 09-Apr-1999 #text_change 11-Jun-1999	text_change 11-Jun-1999
	Righth, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee,	Lee, H.; Dubois, J.; Aldredge, T
	k1, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol, 179, 7135-7155, 1997	P.; Noelling, J.; Reeve, J.N.
	A: Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A; Reference number: A69000; MUID: 98037514; PMID: 9371463	m thermoautotrophicum Delta H: fu 463
	A; Accession: F69022 A; Status: nucleic acid sequence not shown; translation not shown	on not shown
	A; Molecule type: DNA A; Residues: 'MIVRREK', 1-443 <mth></mth>	
	A; Cross-references: GB: AE000885; GB: AE000666; NID: 92622256; PIDN: AAB85657.1; PID: 9262	622256; PIDN:AAB85657.1; PID:g26;
	A) Experimental source: Strain Delta H A; Note: an incorrect initiation codon was used	
	R; Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.	Α.
	Eur. J. Biochem. 194, 6/1-6//, 1990 A;Title: Two genetically distinct methyl-coenzyme M reduc	reductases in Methanobacterium tl
	A; Reference number: S13864; MUID:91099370; PMID:2269306	306
	A; Accession: S/8580	
	A; Residues: 2-15 <ros></ros>	
	A; Experimental source: strain Delta H	
	A; Gene: MTH1168	
	C; Complex: heterohexamer of two alpha (see PIR:B69022), two beta and two gamma (see	2), two beta and two gamma (see 1
	C) Function:	fine w / 2 - / mother   this countries
	A; Pathway: methanogenesis	
	C; Superiamily: metnyl coemizyme m reductase Deta chain C: Keywords: heterohexamer; methanogenesis: oxidoreductase	ctase
	F; 2-443/Product: methyl coenzyme M reductase I beta chain #status experimental F; 367/Active site: Tyr #status predicted	chain #status experimental <mat></mat>
	. c	**************************************
•	11; ches 3	.; Indels 0; Gaps 0;
	Qy 1 NTLKTPRVGGXA 12	
	DD 55 NAEKTAKVGGPA 66	

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A; Molecule type: DNA
A; Residues: 1-704 < DUNN-
B; Residues: 1-704 < DUNN-
B; Residues: 1-704 < DUNN-
B; Residues: 1.704 < 17-535, 1983
C; Mol. Biol. 166, 477-535, 1983
A; Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7
A; Reference number: $44283; MUID: 83241725; PMID: 6864790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: EMBL:V01146; NID:9431187; PIDN:CAA24412.1; PID:915591
C)Comment: T7 DNA polymerase as composed of two chains. One 1s encoded by the phage g
ach chloroplasts can be substituted for the E. coll subunit and the resultant polymer
C;Comment: In addition to polymerase activity, T7 DNA polymerase exhibits a 3' to 5'.
                                                                                                                                                             A;Cross-references: EMBL:274826; NID:91419921; PIDN:CAA99096.1; PID:91419922; MIPS:YO
A;Experimental source: strain S288C
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C'Species: phage T7
C'Date: 13-Jun-1983 *sequence_revision 13-Jun-1983 *text_change 11-Jun-1999
C'Accession: A00716; S42311
R'Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, September 1982
A'Reference number: A94615
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C;Superfamily: phage T7 DNA-directed DNA polymerase phage chain
C;Keywords: DNA binding; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 2; Length 991;
Pred. No. 38;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-directed DNA polymerase (EC 2.7.7.7) phage chain - phage T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 704;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 F)14-10/Domain: transmembrane #status predicted <TM1>
F)95-111/Domain: transmembrane #status predicted <TM2>
F)141-157/Domain: transmembrane #status predicted <TM3>
F)32-408/Domain: transmembrane #status predicted <TM3>
F)392-408/Domain: transmembrane #status predicted <TM4>
F)442-458/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;585-601/Domain: transmembrane #status predicted <TM7>
F;641-657/Domain: transmembrane #status predicted <TM8>
F;665-681/Domain: transmembrane #status predicted <TM9>
                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: yeast probable membrane protein YOL084w C;Reywords: transmembrane protein
   Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1;
Pred. No. 42;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.5%;
                                                                                                                                                                                                                                                                                                      A; Cross-references: SGD: S0005444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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569 NTLATPRMG 577
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289 IKTPKVGG 296
                               A; Reference number: $66775
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   to the Protein
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Best Local Similarity
Matches 6; Conserv
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                                                                                                  A; Molecule type: DNA
A; Residues: 1-991 <ZUW>
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                                                                                                                                                                                                                                                                                                                                         A; Map position: 15L
                                                                      A; Accession: S66778
                                                                                                                                                                                                                                                                       A; Gene: SGD: PHM7
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                                                                                                                       R;Bokranz, M.; Baeumner, G.; Allmansberger, R.; Ankel-Fuchs, D.; Klein, A.
J. Bacteriol. 170, 568-577, 1988
A;Title: Cloning and characterization of the methyl coenzyme M reductase genes from Meth
A;Reference number: A91891; MUID:88115150; PMID:2448287
                                                                                                                                                                                                                                                                                                                                                                                                  Experimental source: strain Marburg. Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.

Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.

Wr. J. Blochem. 194, 871-877, 1990

11tle: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium therm

Reference number: S13864; MUID:91099370; PMID:2269306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contents: annotation; X-ray crystallography, 1.45 angstroms
Complex: heterohexamer of two alpha (see PIR:E28544), two beta and two gamma (see PIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 1-9,'D' <KNA>
Cross-references: GB:X55029; NID:g298118
Cross-references: GB:X55029; NID:g298118
Experimental source: strain Marburg, DSM 2133
Experimental source: strain Marburg, DSM 2133
Experimental sequence in GenBank entry MTWCMR, release 109.0 (PID:g298119) is incomplete Exmler, U.; Grabarse, W.; Shima, S.; Goubeaud, W.; Thauer, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title: Crystal structure of methyl-coenzyme M reductase: the key enzyme of biological Reference number: A58866, MUID:98035783; PMID:9367957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: catalyzes the reaction of methyl coenzyme M (2-(methylthio)enthanesulfon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast 11, 975-986, 1995
A; Title: A 29,425 kb segment on the left arm of yeast chromosome XV contains more than A; Reference number: S57374; MUID:96021609; PMID:8533473
A; Accession: S57385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: methyl coenzyme M reductase beta chain
C;Kayvords: heterohoxamer; methanogenesis; oxidoreductase
F):2-443/Product: methyl coenzyme M reductase I beta chain #status experimental <MAT>
F):367/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:X07794; GB:M18969; NID:944607; PIDN:CAA30635.1; PID:944608
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N;Alternate names: hypothetical protein 00953
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 19-Apr-2002
C;Accession: S57385; S66778; S50421
R;Zumatein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
                                                           Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 11-Jun-1999
Accession: A28544; S78577; S12808
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A;Cross-references: EMBL:X83121; NID:g600461; PIDN:CAA58195.1; PID:g600474
R;Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: not compared with conceptual translation
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Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: protein
Residues: 2-19, /x',21 <ROS>
Experimental source: strain Marburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 66./*,
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pathway: methanogenesis
                                                                                                                                                                                                                                                                                                      Molecule type: DNA
Residues: 1-443 <BOK>
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Residues: 1-9,'D' <
                                                                                                                                                                                                                                                                   Accession: A28544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: S78577
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C; Accession: E85504
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .Cross-references: GB:AE005174; NID:g12512926; PIDN:AAG54497.1; GSPDB:GN00145; UWGP:
Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                        GB:L77117; NID:g1590861; PID:g1590864; TIGR:MJ0081; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein EC80197 [imported] - Escherichia coli (strain 0157:H7, substrain C) Species: Escherichia coli (C) Species: Bscherichia coli (C) Species: 18-011-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 (C) Accession: E90653 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, (Gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shiftle: Complete genome sequence coli 0157:H7 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000007; PIDN:BAB33620.1; PID:g13359653; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80197
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Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                              Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 35;
3; Mismatches 2; Indels
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   A; Reference number: A64300; MUID:96337999; PMID:8688087
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                                                                                                                                                                                                                                                              A;Map position: FOR74658-76013
A;Start codon: TTG
C;Superfamily: methyl coenzyme M reductase beta chain
C;Reywords: methanogenesis; oxidoreductase
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); Pred. No. 35;
3; Mismatches
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red. No. 43;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No.
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54.5%;
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66.7%;
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Best Local Similarity 66.7
Matches 8; Conservative
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|NALKTGAVGGKA 70
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TVRPPRLGGNA
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                                                                 Molecule type: DNA
Residues: 1-451 <Bt
                                           Accession: A64310
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                       C; Species: Lactococcus lactis subsp. lactis
C; Species: Lactococcus lactis subsp. lactis
C; Species: Lactococcus lactis subsp. lactis
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C; Accession: 686767
A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sa A; Reference number: A86625; MuID:21235186; PMID:11337471
A; Reference number: A86625; MuID:21235186; PMID:11337471
A; Reference number: A86625; MuID:21235186; PMID:11337471
A; Residues: 1-257 <STO>
A; Cross-references: GB:AE005176; PID:q12724105; PIDN:AAK05241.1; GSPDB:GN00146
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: yifH
C; Superfamily: nagD protein
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A. A. Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. A. Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschil
N-acetylglucosamine catabolic protein [imported] - Lactococcus lactis subsp. lactis (str
S. Species: Lactococcus lactis subsp. lactis
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C; Accession: G86767
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., I.J. T.H.; Lin, X.; Liu, X.; Liu, X.; Liu, X.; Liu, Z.S.; Liu, Y.; Liu, Y.; Liu, Z.S.; Liu, Y.; Raizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Methanococcus jannaachii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Apr-1999
C;Accession: A64310
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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25;
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1; Mismatches
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Pred. No.
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87.5%;
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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115 TLKTPONGG 123
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47 NTTKTPRV 54
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A; Residues: 1-266 <STO>
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Length 235;

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Length 451;

us-09-743-225-8.rpr

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A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04789.1; GSPDB:GA;Experimental source: strain C-125
C;Genetics:
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C;Specidas: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 03-Feb-2003
C;Accession: H70346
K;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
Vature 392, 353-358, 1998
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A;Expertimental source: strain VF5
C;Genetics:
A;Gene: rfe
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R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A; Reference number: A83650; MUID: 20512582; PMID: 11058132
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A:Accession: H70346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tartrate dehydrogenase BH1070 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-357 <AQF>
submitted to the EMBL Data Library, December 1995
A; Description: The sequence of C. elegans cosmid F38El.
A; Reference number: 221495
A; Recession: T34260
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-310 cGATA
A; Residues: 1-
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54;
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Pred. No. 53;
2; Mismatches
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C;Superfamily: 3-isopropylmalate dehydrogenase
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Pred. No.
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llarity 60.0%;
Conservative
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75.0%;
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183 NKLKTPRV 190
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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A, Molecule type: DNA
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: C64744
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: AG0332
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H.T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-215 <BLAT>
A;Cross-references: GB:AE000128; GB:U00096; NID:91786383; PIDN:AAC73306.1; PID:91786393;
A;Experimental source: strain K-12, substrain MG1655

    Salmonella enterica subsp. enterica

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A, Molecule type: DNA
A, Residues: 1-235 < PAR>
A, Residues: GB: AL513382; PIDN: CAD08703.1; PID: g16501526; GSPDB: GN00176
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C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
C.Accession: T.34260
R.Gattung, S.: Le, T.
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Pred. No. 35;
3; Mismatches 2; Indels
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35;
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                                                                                                                                                                                                                                                                                 yaeB protein - Escherichia coli (strain K-12)
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Pred. No.
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
                                2 TLKTPRVGGXA 12
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74 TVRPPRLGGNA 84
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74 TVRPPRLGGNA 84
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Best Local Similarity
Matches 6; Conserv
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A;Gene: yaeB
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Cross-references: EMBL:X66836; NID:g42941; PIDN:CAA47308.1; PID:g42942
Experimental source: strain Ki2.38
Blattener, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
1.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-410 <BLAT>
A; Cross-references: GB:AE000374; GB:U00096; NID:g1789270; PIDN:AAC75950.1; PID:g1789279;
A; Experimental source: strain K-12, substrain MG1655
C; Comment: The active enzyme is a tetramer of identical chains; it catalyzes the first of oglyceric acid to 3-phosphohydroxypyruvic acid. In bacteria, this enzyme displays feedba
                                                                                                                                                                                                                                                                                                                                                           Tobey, K.L.; Grant, G.A.
1810]. Chem. 261, 12179-12183, 1986
Title: The nucleotide sequence of the serA gene of Escherichia coli and the amino acid
Reference number: A25200; WUID:86304370; PMID:3017965
Accession: A25200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Rex, J.H.; Aronson, B.D.; Somerville, R.L.
Bacteriol. 173, 5944-5953, 1991
'Title: The tdh and serA operons of Escherichia coli: mutational analysis of the regula Reference number: A38156; MUID:92011350; PMID:1917830
Status: preliminary
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                                                                                                                                                                                                                                                   osphoglycerate dehydrogenase (EC 1.1.1.95) - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                             Species: Escherichia coll
Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 01-Mar-2002
Accession: A25200; B38156; S22096; H65075
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ross references: GB:M64630; NID:g147807; PIDN:AAA73016.1; PID:g551837.ioy, I.; Leadlay, P.F. mitted to the EMBL Data Library, June 1992 efference number: S22096 ccession: S22096
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11tle: The complete genome sequence of Escherichia coli K-12.
Reference number: A64720; MUID:97426617; PMID:9278503
Accession: H65078
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61;
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C;Reywords: NAD; oxidoreductase; serine biosynthesis
F;153-181/Region: beta-alpha-beta NAD nucleotide-binding fold
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Pred. No. 61;
1; Mismatches
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Best Local Similarity 60.0%;
Matches 6; Conservative
Conservative
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                                                    5 TPRVGGXA 12
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42 TPRIGGLA 49
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Matches
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Search completed: August 28, 2003, 18:39:06 Job time : 13.2727 secs